

## RAW SEQUENCE LISTING

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Application Serial Number: 10/619,545B  
Source: IFW/b  
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IFW16

## RAW SEQUENCE LISTING

DATE: 03/20/2007

PATENT APPLICATION: US/10/619,545B

TIME: 08:52:55

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Output Set: N:\CRF4\03202007\J619545B.raw

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3 <110> APPLICANT: OLSON, LARS
4     BURVENICH, SILVIA
5     SYDOW, OLOF
6     ANVRET, MARIA
7     ZHANG, ZHIPING
9 <120> TITLE OF INVENTION: ADH7 NUCLEOTIDES
11 <130> FILE REFERENCE: 1522-1001-1
13 <140> CURRENT APPLICATION NUMBER: 10/619,545B
14 <141> CURRENT FILING DATE: 2003-07-16
16 <150> PRIOR APPLICATION NUMBER: PCT/SE99/01136
17 <151> PRIOR FILING DATE: 1999-06-23
19 <150> PRIOR APPLICATION NUMBER: SE 9802294-0
20 <151> PRIOR FILING DATE: 1998-06-26
22 <150> PRIOR APPLICATION NUMBER: 60/090,925
23 <151> PRIOR FILING DATE: 1998-06-26
25 <160> NUMBER OF SEQ ID NOS: 40
27 <170> SOFTWARE: PatentIn Ver. 3.3
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65 <210> SEQ ID NO: 5
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68 <213> ORGANISM: Homo sapiens
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86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 7
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93 <211> LENGTH: 2025
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95 <213> ORGANISM: Homo sapiens
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119 <222> LOCATION: (1311)..(1571)
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126 <221> NAME/KEY: CDS
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129 <220> FEATURE:
130 <221> NAME/KEY: CDS
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140 tctctaaaat cagccatgcc taggcaaagc agcttgcact taaacaccca atacattttt 240
142 catgattgtg ttgaagtga gtaacctaac ccgtttttat atccttcaaa ataaggtgga 300
144 taggaatgct ttcagccctt ttcaatagct ttgattatct tgtttttggt agatccctcc 360
146 tcttggtttg atcatagtag ttactgtatt tctttttata agctggtctg caaagggtag 420
148 ggcttgacaga ccattgcaaa gttgtgacgg ctgtgagtca tattgctgaa ggtggaactc 480
150 tgaagccaga ctatctatgt gaaggcacia gctgctgtta tatacaacag agtgaactga 540
152 gcatcagtca gaaaaagtct atgtttgcag aaatacagat ccaagacaaa gacagg atg 599
153 Met
154 1
156 ggc act gct gga aaa gtaagtggaa cttttttgcc tttttcttag gtt att aaa 653
157 Gly Thr Ala Gly Lys Val Ile Lys
158 5
160 tgc aaa gca gct gtg ctt tgg gag cag aag caa ccc ttc tcc att gag 701
161 Cys Lys Ala Ala Val Leu Trp Glu Gln Lys Gln Pro Phe Ser Ile Glu
162 10 15 20 25
164 gaa ata gaa gtt gcc cca cca aag act aaa gaa gtt cgc att aag 746
165 Glu Ile Glu Val Ala Pro Pro Lys Thr Lys Glu Val Arg Ile Lys
166 30 35 40
168 gtaagcgtga gcccttgtct ttgaacacag att ttg gcc aca gga atc tgt cgc 800
169 Ile Leu Ala Thr Gly Ile Cys Arg
170 45
172 aca gat gac cat gtg ata aaa gga aca atg gtg tcc aag ttt cca gtg 848
173 Thr Asp Asp His Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val
174 50 55 60
176 att gtg gga cat gag gca act ggg att gta gag agc att gga gaa gga 896
177 Ile Val Gly His Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly
178 65 70 75 80
180 gtg act aca gtg aaa cca g gtatatgcag gtgtcatttt tttcctgtag gt gac 950
181 Val Thr Thr Val Lys Pro Gly Asp
182 85
184 aaa gtc atc cct ctc ttt ctg cca caa tgt aga gaa tgc aat gct tgt 998
185 Lys Val Ile Pro Leu Phe Leu Pro Gln Cys Arg Glu Cys Asn Ala Cys
186 90 95 100
188 cgc aac cca gat ggc aac ctt tgc att agg agc ga gtaggtttca 1043
189 Arg Asn Pro Asp Gly Asn Leu Cys Ile Arg Ser Asp
190 105 110 115
192 gtcattgatg tatcaaacag t att act ggt cgt gga gta ctg gct gat ggc 1094
193 Ile Thr Gly Arg Gly Val Leu Ala Asp Gly
194 120 125
196 acc acc aga ttt aca tgc aag ggc aaa cca gtc cac cac ttc atg aac 1142
197 Thr Thr Arg Phe Thr Cys Lys Gly Lys Pro Val His His Phe Met Asn
198 130 135 140
200 acc agt aca ttt acc gag tac aca gtg gtg gat gaa tct tct gtt gct 1190
201 Thr Ser Thr Phe Thr Glu Tyr Thr Val Val Asp Glu Ser Ser Val Ala
202 145 150 155
204 aag att gat gat gca gct cct cct gag aaa gtc tgt tta att ggc tgt 1238
205 Lys Ile Asp Asp Ala Ala Pro Pro Glu Lys Val Cys Leu Ile Gly Cys

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208 ggg ttt tcc act gga tat ggc gct gct gtt aaa act ggc aag      1280
209 Gly Phe Ser Thr Gly Tyr Gly Ala Ala Val Lys Thr Gly Lys
210 175      180      185
212 gtaagaaaca gggtacattc ctctccacag gtc aaa cct ggt tcc act tgc gtc      1334
213      Val Lys Pro Gly Ser Thr Cys Val
214      190      195
216 gtc ttt ggc ctg gga gga gtt ggc ctg tca gtc atc atg ggc tgt aag      1382
217 Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val Ile Met Gly Cys Lys
218      200      205      210
220 tca gct ggt gca tct agg atc att ggg att gac ctc aac aaa gac aaa      1430
221 Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu Asn Lys Asp Lys
222      215      220      225
224 ttt gag aag gcc atg gct gta ggt gcc act gag tgt atc agt ccc aag      1478
225 Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys Ile Ser Pro Lys
226      230      235      240
228 gac tct acc aaa ccc atc agt gag gtg ctg tca gaa atg aca ggc aac      1526
229 Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu Met Thr Gly Asn
230 245      250      255      260
232 aac gtg gga tac acc ttt gaa gtt att ggg cat ctt gaa acc atg      1571
233 Asn Val Gly Tyr Thr Phe Glu Val Ile Gly His Leu Glu Thr Met
234      265      270      275
236 gtaagacccc aaaatccggtt ttaaactcag att gat gcc ctg gca tcc tgc cac      1625
237      Ile Asp Ala Leu Ala Ser Cys His
238      280
240 atg aac tat ggg acc agc gtg gtt gta gga gtt cct cca tca gcc aag      1673
241 Met Asn Tyr Gly Thr Ser Val Val Val Gly Val Pro Pro Ser Ala Lys
242      285      290      295
244 atg ctc acc tat gac ccg atg ttg ctc ttc act gga cgc aca tgg aag      1721
245 Met Leu Thr Tyr Asp Pro Met Leu Leu Phe Thr Gly Arg Thr Trp Lys
246 300      305      310      315
248 gga tgt gtc ttt gga g gtcaggaaag caaagtgtgc ttatttgcag gt ttg aaa      1775
249 Gly Cys Val Phe Gly      Gly Leu Lys
250      320
252 agc aga gat gat gtc cca aaa cta gtg act gag ttc ctg gca aag aaa      1823
253 Ser Arg Asp Asp Val Pro Lys Leu Val Thr Glu Phe Leu Ala Lys Lys
254      325      330      335
256 ttt gac ctg gac cag ttg ata act cat gtt tta cca ttt aaa aaa atc      1871
257 Phe Asp Leu Asp Gln Leu Ile Thr His Val Leu Pro Phe Lys Lys Ile
258 340      345      350      355
260 agt gaa gga ttt gag ctg ctc aat tca gga caa ag gtaactgttt      1916
261 Ser Glu Gly Phe Glu Leu Leu Asn Ser Gly Gln Ser
262      360      365
264 cttatcattt tacatttcag c att cga acg gtc ctg acg ttt tgagatccaa      1968
265      Ile Arg Thr Val Leu Thr Phe
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268 agtggcagga ggtctgtgtt gtcattggtga actggagttt ctcttgtgag agttccc      2025
271 <210> SEQ ID NO: 9
272 <211> LENGTH: 374

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273 &lt;212&gt; TYPE: PRT

274 &lt;213&gt; ORGANISM: Homo sapiens

276 &lt;400&gt; SEQUENCE: 9

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281           20           25           30
283 Lys Thr Lys Glu Val Arg Ile Lys Ile Leu Ala Thr Gly Ile Cys Arg
284           35           40           45
286 Thr Asp Asp His Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val
287           50           55           60
289 Ile Val Gly His Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly
290   65           70           75           80
292 Val Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Leu Pro
293           85           90           95
295 Gln Cys Arg Glu Cys Asn Ala Cys Arg Asn Pro Asp Gly Asn Leu Cys
296           100          105          110
298 Ile Arg Ser Asp Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr
299           115          120          125
301 Arg Phe Thr Cys Lys Gly Lys Pro Val His His Phe Met Asn Thr Ser
302           130          135          140
304 Thr Phe Thr Glu Tyr Thr Val Val Asp Glu Ser Ser Val Ala Lys Ile
305  145           150           155           160
307 Asp Asp Ala Ala Pro Pro Glu Lys Val Cys Leu Ile Gly Cys Gly Phe
308           165          170          175
310 Ser Thr Gly Tyr Gly Ala Ala Val Lys Thr Gly Lys Val Lys Pro Gly
311           180          185          190
313 Ser Thr Cys Val Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val Ile
314           195          200          205
316 Met Gly Cys Lys Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu
317           210          215          220
319 Asn Lys Asp Lys Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys
320  225           230          235          240
322 Ile Ser Pro Lys Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu
323           245          250          255
325 Met Thr Gly Asn Asn Val Gly Tyr Thr Phe Glu Val Ile Gly His Leu
326           260          265          270
328 Glu Thr Met Ile Asp Ala Leu Ala Ser Cys His Met Asn Tyr Gly Thr
329           275          280          285
331 Ser Val Val Val Gly Val Pro Pro Ser Ala Lys Met Leu Thr Tyr Asp
332           290          295          300
334 Pro Met Leu Leu Phe Thr Gly Arg Thr Trp Lys Gly Cys Val Phe Gly
335  305           310          315          320
337 Gly Leu Lys Ser Arg Asp Asp Val Pro Lys Leu Val Thr Glu Phe Leu
338           325          330          335
340 Ala Lys Lys Phe Asp Leu Asp Gln Leu Ile Thr His Val Leu Pro Phe
341           340          345          350
343 Lys Lys Ile Ser Glu Gly Phe Glu Leu Leu Asn Ser Gly Gln Ser Ile
344           355          360          365

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**VERIFICATION SUMMARY**

DATE: 03/20/2007

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